

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: November 4, 2005, 12:01:00 ; Search time 13047 Seconds
(without alignments)
1.752 Million cell updates/sec

Title: US-09-982-091A-5

Perfect score: 58837

Sequence: 1 aagcagcagcttcaact.....tatgcagcagctccctcag 58837

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 194296 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : a1354864.gb.pr.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58837	100.0	194296	1	AL354864 ACCSSION:AL354864
2	558.173	0.9	194296	1	AL354864 ACCSSION:AL354864

ALIGNMENTS

RESULT 1
AL354864
LOCUS 194296 bp DNA linear PRI 04-APR-2001
DEFINITION Human DNA sequence from clone RPI1-435D7 on chromosome 1. Contains ESTs, STSs, GSSs and Cpg Islands. Contains a novel gene and the 5' part of the PSMB2 gene for proteasome (prosome, macropain) subunit 2, beta type, complete sequence.

ACCESSION AL354864
VERSION AL354864.16 GI:10185566
KEYWORDS HTG; Cpg island; macropain; prosome; proteasome; PSMB2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 194296)
AUTHORS Howden, P.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1BA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Sep 19, 2000 this sequence version replaced gi:9714820.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with

FEATURES

source

Only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL, Sw: SWISSPROT, Tr: TREMBL, Wp: WORMPEP, Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
This sequence is the entire insert of clone RPI1-435D7 The true left end of clone RPI1-62B3 is at 123829 in this sequence. The true right end of clone RPI1-555P23 is at 81044 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unseq' feature key. RPI1-435D7 is from the library RPI1-11.2 constructed by the group of Pletier de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6.

Location/Qualifiers
1..194296
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RPI1-435D7"
/clone_1fb="RPI1-11.2"
72..131
/note="15 copies 4 mer cctt 78% conserved"
2010..2057
/note="24 copies 2 mer tt 75% conserved"
2353..2650
/note="A1uSg1 repeat: matches 1..301 of consensus"
5390..6351
/note="Cpg island"
/evidence="not_experimental"
7263..7656
/note="MUT1B repeat: matches 1..390 of consensus"
8017..8605
/note="Cpg island"
/evidence="not_experimental"

repeat_region
11677..12004
/note="LIMB6 repeat: matches 5474..5827 of consensus"
12328..12620
/note="LIMB6 repeat: matches 5188..5474 of consensus"
12659..13001
/note="LIMB6 repeat: matches 4844..5199 of consensus"
13304..13326
/note="LIMB6 repeat: matches 4822..4844 of consensus"
13627..13881
/note="LIMB6 repeat: matches 4601..4822 of consensus"
13883..13938
/note="28 copies 2 mer tg 96% conserved"
14265..14436
/note="LIMB6 repeat: matches 4442..4609 of consensus"
14734..14909
/note="LIMB6 repeat: matches 4265..4442 of consensus"
14919..14956
/note="LIMB6 repeat: matches 4197..4265 of consensus"
14957..14986
/note="LIMB6 repeat: matches 4243..4276 of consensus"
15300..15341
/note="LIMB6 repeat: matches 4197..4243 of consensus"
15639..16080
/note="LIMB6 repeat: matches 5714..6155 of consensus"
16081..16208
/note="LIMB6 repeat: matches 4103..4197 of consensus"
17572..17808
/note="MUT1B repeat: matches 3..221 of consensus"
18105..18136
repeat_region